# Figure 1

```
         1              10             20             30
         *              *              *              *
G AATTCCGCTA CTACTCAACA ATG AAG ATG CTT TAC GCT ATC GCT
                        Met Lys Met Leu Tyr Ala Ile Ala

    40             50             60             70
    *              *              *              *
ATA ATG TTT CTC CTG GTA TCA TTA TGC AGC GCA AGA ACA GTG
Ile Met Phe Leu Leu Val Ser Leu Cys Ser Ala Arg Thr Val

80             90             100            110            120
*              *              *              *              *
AGG AAG GCA TAC CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC
Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp

         130            140            150            160
         *              *              *              *
GAC TGT GGA ACT CAG AAG CCA TGC GAG GCC AAG TGC AAT GAG
Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu

    170            180            190            200
    *              *              *              *
GAA CCC CCT GAG GAG GAA GAT CCG ATA TGC CGC TCA CGT GGT
Glu Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly

    210            220            230            240
    *              *              *              *
TGT TTA TTA CCT CCT GCT TGC GTA TGC AAA GAC GGA TTC TAC
Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr

    250            260            270            280
    *              *              *              *
AGA GAC ACG GTG ATC GGC GAC TGT GTT AGG GAA GAA GAA TGC
Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Glu Cys

290            300            310            320            330
*              *              *              *              *
GAC CAA CAT GAG ATT ATA CAT GTC TGA ACGAGAAAGC AACAATAACC
Asp Gln His Glu Ile Ile His Val

    340            350            360            370            380
    *              *              *              *              *
AAAGGTTCCA ACTCTCGCTC TGCAAAATCG CTAGTTGGAT GTCTCTTTTG

    390            400            410            420            430
    *              *              *              *              *
CGTCCGAATA GTTTTAGTTG ATGTTAAGTA AGAACTCCTG CTGGAGAGAA

    440            450
    *              *
TAAAGCTTTC CAACTCC poly(A)
```

# Figure 2

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp
1               5                   10

Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu Glu
15              20                  25

Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly Cys
    30              35                  40

Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg
        45              50                  55

Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Glu Cys Asp
            60              65                  70

Gln His Glu Ile Ile His Val
            75

# Figure 3

```
        1                  10                 20                 30
        *                  *                  *                  *
G AATTCCGCTA CTACTCAACA ATG AAG ATG CTT TAC GCT ATC GCT
                         Met Lys Met Leu Tyr Ala Ile Ala

   40                 50            60                 70
   *                  *             *                  *
ATA ATG TTT CTC CTG GTG TCA TTA TGC AGC ACA AGA ACA GTG
Ile Met Phe Leu Leu Val Ser Leu Cys Ser Thr Arg Thr Val

80                 90            100                110                120
*                  *             *                  *                  *
AGG AAG GCA TAC CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC
Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp

           130            140            150            160
           *              *              *              *
GTC TGT GGA ACT AAG AAG CCA TGC GAG GCC AAG TGC AGT GAG
Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu

        170            180            190            200
        *              *              *              *
GAA GAG GAG GAA GAT CCG ATA TGC CGA TCA TTT TCT TGT CCG
Glu Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro

        210            220            230            240
        *              *              *              *
GGT CCC GCT GCT TGC GTA TGC GAA GAC GGA TTC TAC AGA GAC
Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp

   250            260            270            280
   *              *              *              *
ACG GTG ATC GGC GAC TGT GTT AAG GAA GAA GAA TGC GAC CAA
Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys Asp Gln

290            300            310            320            330
*              *              *              *              *
CAT GAG ATT ATT CAT GTC TGA ACGAGAGAGC AGTAATAACC
His Glu Ile Ile His Val

           340            350            360            370            380
           *              *              *              *              *
AAAGGTTCCA ACTTTCGCTC TACAAAATCG CTAGTTGGAT TTCTCCTTTG

           390            400            410            420            430
           *              *              *              *              *
CGTGCGAATA GTTTTAGTTG ATATTAAGTA AAACCTCCTG TTGAAGAGAA

           440
           *
TAAAGCTTTC CAACTTC poly(A)
```

# Figure 4

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Val
1           5               10

Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu
15              20              25

Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly
    30              35              40

Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr
    45              50              55

Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys Asp Gln His
        60              65              70

Glu Ile Ile His Val
        75

# Figure 5

Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu
            1         5             10

Trp Leu Asp Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys
            15             20

Cys Asn Glu Glu Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg
25             30             35

Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp
    40             45             50

Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu
        55             60             65

Glu Glu Cys Asp Gln His Glu Ile Ile His Val
            70             75

# Figure 6

Arg Thr Val Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu
              1           5               10

Trp Leu Asp Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys
              15          20

Cys Ser Glu Glu Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe
25              30              35

Ser Cys Pro Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe
    40          45              50

Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu
    55          60              65

Cys Asp Gln His Glu Ile Ile His Val
        70              75

# Figure 7A-1

```
  1          10          20                  30                  40
  *          *           *                   *                   *
GAATTCACTA TTATCCAACA ATG GCG GTG CTT TAT TCA GTA GCA
EcoRI                  Met Ala Val Leu Tyr Ser Val Ala

     50          60          70          80
     *           *           *           *
ATA GCG TTA CTA CTG GTA TCA CAA TGC AGT GGG AAA CCG AAC
Ile Ala Leu Leu Leu Val Ser Gln Cys Ser Gly Lys Pro Asn

     90          100         110         120
     *           *           *           *
AAT GTG ATG ACT AAC GCT TGT GGT CTT AAT GAA TAT TTC GCT
Asn Val Met Thr Asn Ala Cys Gly Leu Asn Glu Tyr Phe Ala

130         140         150         160         170
  *           *           *           *           *
GAG TGT GGC AAT ATG AAG GAA TGC GAG CAC AGA TGC AAT GAG
Glu Cys Gly Asn Met Lys Glu Cys Glu His Arg Cys Asn Glu

          180         190         200         210
            *           *           *           *
GAG GAA AAT GAG GAA AGG GAC GAG GAA AGA ATA ACG GCA TGC
Glu Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile Thr Ala Cys

          220         230         240         250
            *           *           *           *
CTC ATC CGT GTG TGT TTC CGT CCT GGT GCT TGC GTA TGC AAA
Leu Ile Arg Val Cys Phe Arg Pro Gly Ala Cys Val Cys Lys

          260         270         280         290
            *           *           *           *
GAC GGA TTC TAT AGA AAC AGA ACA GGC AGC TGT GTG GAA GAA
Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser Cys Val Glu Glu

          300         310         320         330
            *           *           *           *
GAT GAC TGC GAG TAC GAG AAT ATG GAG TTC ATT ACT TTT GCA
Asp Asp Cys Glu Tyr Glu Asn Met Glu Phe Ile Thr Phe Ala

340         350         360         370         380
  *           *           *           *           *
CCA GAA GTA CCG ATA TGT GGT TCC AAC GAA AGG TAC TCC GAC
Pro Glu Val Pro Ile Cys Gly Ser Asn Glu Arg Tyr Ser Asp

          390         400         410         420
            *           *           *           *
TGC GGC AAT GAC AAA CAA TGC GAG CGC AAA TGC AAC GAG GAC
Cys Gly Asn Asp Lys Gln Cys Glu Arg Lys Cys Asn Glu Asp

          430         440         450         460
            *           *           *           *
GAT TAT GAG AAG GGA GAT GAG GCA TGC CGC TCA CAT GTT TGT
Asp Tyr Glu Lys Gly Asp Glu Ala Cys Arg Ser His Val Cys
```

# Figure 7A-2

```
        470              480              490              500
         *                *                *                *
GAA CGT CCT GGT GCC TGT GTA TGC GAA GAC GGG TTC TAC AGA
Glu Arg Pro Gly Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg

        510              520              530          540
         *                *                *            *
AAC AAA AAA GGT AGC TGT GTG GAA AGC GAT GAC TGC GAA TAC
Asn Lys Lys Gly Ser Cys Val Glu Ser Asp Asp Cys Glu Tyr

550          560               570          580          590
 *            *                 *            *             *
GAT AAT ATG GAT TTC ATC ACT TTT GCA CCA GAA ACC TCA CGA
Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu Thr Ser Arg

          600              610            620          630          640
           *                *              *            *            *
TAA CCAAAGATGC TACCTCTCGT ACGCAACTCC GCTGATTGAGGTTGATTC

          650              660            670          680          690
           *                *              *            *            *
ACTCCCTTGCATCTCAACATTTTTTTTGTGATGCTGTGCATCTGAGCTTAACCTG

700          710
 *            *
ATAAAGCCTATGGTG poly(A)
```

# Figure 7B

```
1           10              20              30              40
*           *               *               *               *
GAATTCCGC ATG CGG ACG CTC TAC CTC ATT TCT ATC TGG TTG
EcoRI     Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu

          50              60              70          80
          *               *               *           *
TTC CTC ATC TCG CAA TGT AAT GGA AAA GCA TTC CCG AAA TGT
Phe Leu Ile Ser Gln Cys Asn Gly Lys Ala Phe Pro Lys Cys

          90              100             110         120
          *               *               *           *
GAC GTC AAT GAA AGA TTC GAG GTG TGT GGC AAT CTG AAG GAG
Asp Val Asn Glu Arg Phe Glu Val Cys Gly Asn Leu Lys Glu

      130             140             150             160
      *               *               *               *
TGC GAG CTC AAG TGC GAT GAG GAC CCT AAG ATA TGC TCT CGT
Cys Glu Leu Lys Cys Asp Glu Asp Pro Lys Ile Cys Ser Arg

170             180             190             200             210
*               *               *               *               *
GCA TGT ATT CGT CCC CCT GCT TGC GTA TGC GAT GAC GGA TTC
Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp Asp Gly Phe

          220             230             240         250
          *               *               *           *
TAC AGA GAC AAA TAT GGC TTC TGT GTT GAA GAA GAC GAA TGT
Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu Asp Glu Cys

          260             270             280         290
          *.              *               *           *
AAC GAT ATG GAG ATT ATT ACT TTT CCA CCA GAA ACC AAA TGA
Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys

      300         310         320         330         340
      *           *           *           *           *
TGACCGAAGC TTCCACCTTT CTATACATAT CTTCACTGCTTGACAGGCTTCT

350         360         370         380         390         400
*           *           *           *           *           *
CGACAATTTAGAAGTTCTGCTTGACTTTGTCTATTTGAAATTGTTCACACTAATG

      410         420
      *           *
GGGGAAGTAAAGCATTTTCACGAC poly(A)
```

# Figure 7C

```
1              10             20             30             40
*               *              *              *              *
GAATTCCGCT ACATTTTCAA CA ATG TCG ACG CTT TAT GTT ATC
EcoRI                    Met Ser Thr Leu Tyr Val Ile


        50             60             70             80
         *              *              *              *
GCA ATA TGT TTG CTG CTT GTT TCG CAA TGC AAT GGA AGA ACG
Ala Ile Cys Leu Leu Leu Val Ser Gln Cys Asn Gly Arg Thr


        90            100            110            120
         *              *              *              *
GTG AAG AAG TGT GGC AAG AAT GAA AGA TAC GAC GAC TGT GGC
Val Lys Lys Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly


130            140            150            160
 *              *              *              *
AAT GCA AAG GAC TGC GAG ACC AAG TGC GGT GAA GAG GAA AAG
Asn Ala Lys Asp Cys Glu Thr Lys Cys Gly Glu Glu Glu Lys


170            180            190            200            210
 *              *              *              *              *
GTG TGC CGT TCG CGT GAG TGT ACT AGT CCT GGT GCC TGC GTA
Val Cys Arg Ser Arg Glu Cys Thr Ser Pro Gly Ala Cys Val


        220            230            240            250
         *              *              *              *
TGC GAA CAA GGA TTC TAC AGA GAT CCG GCT GGC GAC TGT GTC
Cys Glu Gln Gly Phe Tyr Arg Asp Pro Ala Gly Asp Cys Val


        260            270            280            290
         *              *              *              *
ACT GAT GAA GAA TGT GAT GAA TGG AAC AAT ATG GAG ATC ATT
Thr Asp Glu Glu Cys Asp Glu Trp Asn Asn Met Glu Ile Ile


        300            310            320            330            340
         *              *              *              *              *
ACT ATG CCA AAA CAG TAG TGCGAAGTTC CCTTCTTTCT CCAAATCTG
Thr Met Pro Lys Gln


        350            360            370            380            390
         *              *              *              *              *
C TCCGTGCTCAATTATCACACACCTCCACTAGTTAAGATTGACTGACTCTCTTG


400            410            420            430            440            450
 *              *              *              *              *              *
CATTGTAGTATTTTCGCTTGACTCTGTGCATTTAAGCATGAGATACTACTAGGGA


        460            470
         *              *
GAATAAAAATTACTAACTAC poly(A)
```

## Figure 7D

```
 1           10               20               30               40
 *            *                *                *                *
GAATTCCGG AAA TGT CCT ACC GAT GAA TGG TTC GAT TGG TGT
EcoRI     Lys Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys

             50               60               70          80
              *                *                *           *
GGA ACT TAC AAG CAT TGC GAA CTC AAG TGC GAT AGG GAG CTA
Gly Thr Tyr Lys His Cys Glu Leu Lys Cys Asp Arg Glu Leu

         90              100              110          120
          *                *                *           *
ACT GAG AAA GAA GAG CAG GCA TGT CTC TCA CGT GTT TGT GAG
Thr Glu Lys Glu Glu Gln Ala Cys Leu Ser Arg Val Cys Glu

     130              140              150              160
      *                *                *                *
AAG TCC GCT TGC GTA TGC AAT GAC GGA TTA TAC AGA GAC AAG
Lys Ser Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Lys

170              180              190              200          210
 *                *                *                *           *
TTT GGC AAC TGT GTT GAA AAA GAC GAA TGC AAC GAT ATG GAG
Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu

             220              230              240          250
              *                *                *           *
ATT ATT ACT TTT GCA CCA GAA ACC AAA TAA TGGCCTAAGG TTCC
Ile Ile Thr Phe Ala Pro Glu Thr Lys

         260              270              280          290          300
          *                *                *           *            *
AAACCT TGCTACACAC CGTCAGTGCTTTACTGTTTCCTCTACGTGTTAGTAGT

310          320              330          340          350          360
 *            *                *            *            *            *
TTTGCTTGACTCTGTGTATTTAAGCATTGTCTACTAATGGGCAAAGTAAAGCATT

     370          380          390
      *            *            *
GTAAGGACATAATAATGAGTAAACCTTCTGATTT poly(A)
```

# Figure 7E-1

```
1          10             20                  30               40
*          *              *                   *                *
GAATTCCGGG CGGCAGAAAG ATG CGA ATG CTC TAC CTT GTT CCT
EcoRI                   Met Arg Met Leu Tyr Leu Val Pro

     50             60                  70             80
     *              *                   *              *
ATC TGG TTG CTG CTC ATT TCG CTA TGC AGT GGA AAA GCT GCG
Ile Trp Leu Leu Leu Ile Ser Leu Cys Ser Gly Lys Ala Ala

     90             100                 110            120
     *              *                   *              *
AAG AAA TGT GGT CTC AAT GAA AGG CTG GAC TGT GGC AAT CTG
Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn Leu

130            140                 150            160            170
*              *                   *              *              *
AAG CAA TGC GAG CCC AAG TGC AGC GAC TTG GAA AGT GAG GAG
Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu

          180             190                 200            210
          *               *                   *              *
TAT GAG GAG GAA GAT GAG TCG AAA TGT CGA TCA CGT GAA TGT
Tyr Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys

     220            230                 240            250
     *              *                   *              *
TCT CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC TAC AGA AAC
Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn

     260            270                 280            290
     *              *                   *              *
AAG AAG GGC AAG TGT GTT GCA AAA GAT GTT TGC GAG GAC GAC
Lys Lys Gly Lys Cys Val Ala Lys Asp Val Cys Glu Asp Asp

300            310                 320            330
*              *                   *              *
AAT ATG GAG ATT ATC ACT TTT CCA CCA GAA GAC GAA TGT GGT
Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Glu Cys Gly

340            350                 360            370            380
*              *                   *              *              *
CCC GAT GAA TGG TTC GAC TAC TGT GGA AAT TAT AAG AAG TGC
Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys Lys Cys

          390             400                 410            420
          *               *                   *              *
GAA CGC AAG TGC AGT GAG GAG ACA AGT GAG AAA AAT GAG GAG
Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Glu

          430             440                 450            460
          *               *                   *              *
GCA TGC CTC TCT CGT GCT TGT ACT GGT CGT GCT TGC GTA TGC
Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys
```

## Figure 7E-2

```
     470              480              490              500
      *                *                *                *
AAA GAC GGA TTG TAC AGA GAC GAC TTT GGC AAC TGT GTT CCA
Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro

     510              520              530              540
      *                *                *                *
CAT GAC GAA TGC AAC GAT ATG GAG ATC ATC ACT TTT CCA CCG
His Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro

  550           560           570           580           590
   *             *             *             *             *
GAA ACC AAA CAT TGA CCAGAGGCTC CAACTCTCGC TACACAACGT CA
Glu Thr Lys His

   600           610           620           630           640        650
    *             *             *             *             *          *
GGGCTAGAATGGCCCCTCTGCGAGTTAGTAGTTTTGCTTGACTCTGCTTATTTGA

         660           670           680
          *             *             *
GCACTTTCTATTGATGGCGAAAATAAAGCATTTAAAAC poly(A)
```

# Figure 7F

```
     1          10          20          30          40
     *           *           *           *           *
    GAATTCCGCG CACCTGAGAG GTGAGCTACG CAAGTCTTCG CTGGTACA
    EcoRI
```

```
50              60              70          80              90
 *               *               *           *               *
ATG ATC CGA AAG CTC GTT CTG CTG ACT GCT ATC GTC ACG GTG
Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Thr Val
```

```
            100             110         120             130
             *               *           *               *
GTG CTA AGT GCG AAG ACC TGT GGA CCA AAC GAG GAG TAC ACT
Val Leu Ser Ala Lys Thr Cys Gly Pro Asn Glu Glu Tyr Thr
```

```
        140             150             160         170
         *               *               *           *
GAA TGC GGG ACG CCA TGC GAG CCG AAG TGC AAT GAA CCG ATG
Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Glu Pro Met
```

```
        180             190             200         210
         *               *               *           *
CCA GAC ATC TGT ACT CTG AAC TGC ATC GTG AAC GTG TGT CAG
Pro Asp Ile Cys Thr Leu Asn Cys Ile Val Asn Val Cys Gln
```

```
    220             230             240         250
     *               *               *           *
TGC AAA CCC GGC TTC AAG CGC GGA CCG AAA GGA TGC GTC GCC
Cys Lys Pro Gly Phe Lys Arg Gly Pro Lys Gly Cys Val Ala
```

```
260             270         280         290         300
 *               *           *           *           *
CCC GGA CCA GGC TGT AAA TAG TTCTCCACCT GCCCTTTCGT TGGAA
Pro Gly Pro Gly Cys Lys
```

```
    310         320         330         340
     *           *           *           *
CAAAT GGCTGTCTTTTTACATTCTGAATCAATAAAGCCGAACGGT poly(A)
```

# Figure 8A

```
1            10            20            30            40
*            *             *             *             *
AAGCTTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT
HindIII                                        Met Pro Val

50            60            70            80            90
*            *             *             *             *
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu

              100           110           120           130
              *             *             *             *
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys

              140           150           160           170
              *             *             *             *
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala

              180           190           200           210
              *             *             *             *
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser

220           230           240           250
*             *             *             *
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val

260           270           280           290           300
*             *             *             *             *
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val

              310           320           330           340
              *             *             *             *
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys

              350           360           370           380
              *             *             *             *
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly

              390           400           410           420           430
              *             *             *             *             *
TCA GGC GGA GGCCAAGTCGGCC ATCCCATATCAC GCGGCCGC GGATCC
Ser Gly Gly      SfiI                   NotI     BamHI
```

## Figure 8B

```
 1          10          20          30          40
 *           *           *           *           *
 AAGCTTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT
 HindIII                                      Met Pro Val

 50          60          70          80          90
 *           *           *           *           *
 CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT
 Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu

             100         110         120         130
              *           *           *           *
 CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG
 Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys

             140         150         160         170
              *           *           *           *
 GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT
 Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala

             180         190         200         210
              *           *           *           *
 CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT
 Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser

 220         230         240         250
  *           *           *           *
 GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT
 Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val

 260         270         280         290         300
  *           *           *           *           *
 CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT
 Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val

             310         320         330         340
              *           *           *           *
 ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA
 Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys

             350         360         370         380
              *           *           *           *
 CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC
 Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly

             390         400         410         420         430
              *           *           *           *           *
 TCA GGC GGA G GGCCAAGTCGGCC ATCCCATATCAC GCGGCCGC GGATCC
 Ser Gly Gly      SfiI                     NotI     BamHI
```

## Figure 8C

```
1          10              20            30              40
*           *               *             *               *
AAGCTTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT
HindIII                                      Met Pro Val

50              60              70            80              90
*               *               *             *               *
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu

           100             110           120             130
            *               *             *               *
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys

           140             150           160             170
            *               *             *               *
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala

           180             190           200             210
            *               *             *               *
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser

220             230             240           250
 *               *               *             *
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val

260             270             280           290             300
 *               *               *             *               *
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val

           310             320           330             340
            *               *             *               *
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys

           350             360           370             380
            *               *             *               *
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly

           390             400           410     420         430
            *               *             *       *           *
TCA GGC GGA TC GGCCAAGTCGGCC ATCCCATATCAC GCGGCCGC GGATCC
Ser Gly Gly        SfiI                    NotI     BamHI
```

# Figure 9

```
1            10             20             30             40
*             *              *              *              *
GAATTCCGG CTG GTW TCC TAC TGC AGT GGA AAA GCA ACG ATG
EcoRI     Leu Val Ser Tyr Cys Ser Gly Lys Ala Thr Met

        50             60             70             80
         *              *              *              *
CAG TGT GGT GAG AAT GAA AAG TAC GAT TCG TGC GGT AGC AAG
Gln Cys Gly Glu Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys

        90            100            110            120
         *              *              *              *
GAG TGC GAT AAG AAG TGC AAA TAT GAC GGA GTT GAG GAG GAA
Glu Cys Asp Lys Lys Cys Lys Tyr Asp Gly Val Glu Glu Glu

    130            140            150            160
     *              *              *              *
GAC GAC GAG GAA CCT AAT GTG CCA TGC CTA GTA CGT GTG TGT
Asp Asp Glu Glu Pro Asn Val Pro Cys Leu Val Arg Val Cys

170            180            190            200            210
 *              *              *              *              *
CAT CAA GAT TGC GTA TGC GAA GAA GGA TTC TAT AGA AAC AAA
His Gln Asp Cys Val Cys Glu Glu Gly Phe Tyr Arg Asn Lys

        220            230            240            250
         *              *              *              *
GAT GAC AAA TGT GTA TCA GCA GAA GAC TGC GAA CTT GAC AAT
Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu Leu Asp Asn

        260            270            280            290
         *              *              *              *
ATG GAC TTT ATA TAT CCC GGA ACT CGA AAC TGA ACGAAGGCTC
Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn

    300        310        320        330        340
     *          *          *          *          *
CATTCTTGCT GCACAAGATC GATTGTCTCTCCCCTGCATCTCAGTAGTTTTGC

350        360        370        380        390        400
 *          *          *          *          *          *
TACATTGTATATGGTAGCAAAAAATTAGCTTAGGGAGAATAAAATCTTTACCTAT

    410        420        430
     *          *          *
ATTTAATCAATGAAGTATTCTCTTTCT poly(A)
```
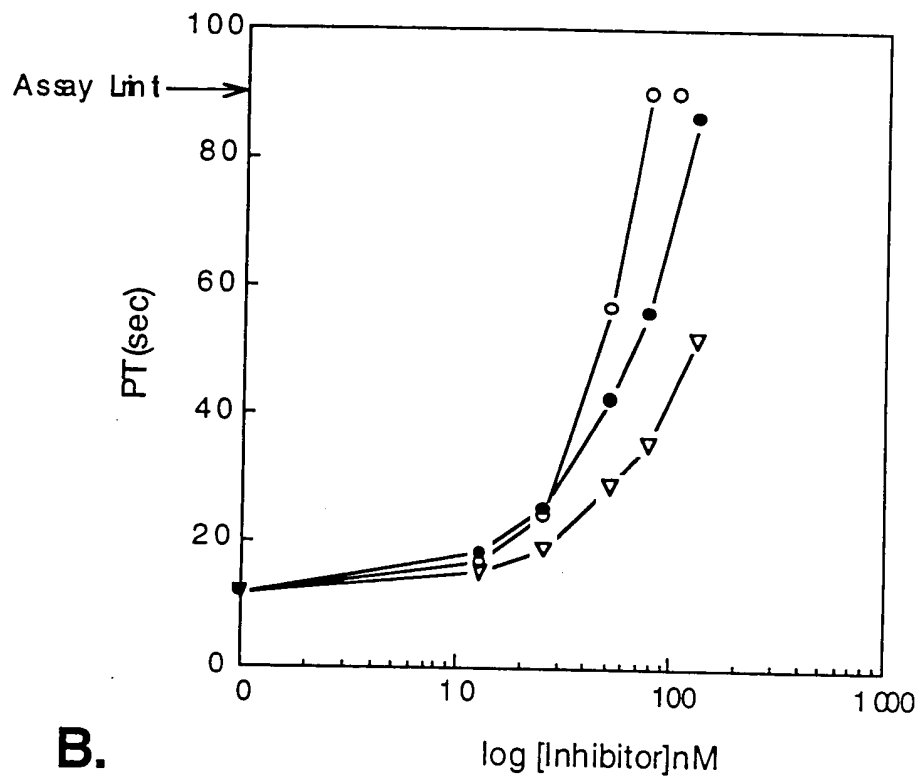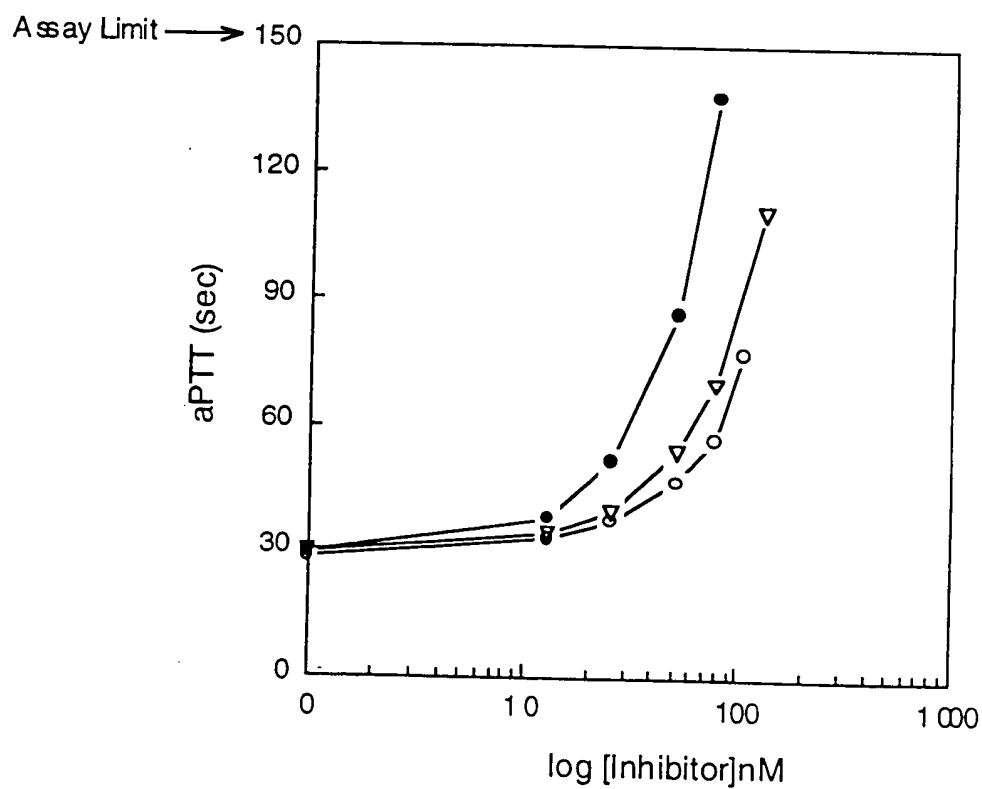
Figure 10

A.



B.

# Figure 11-1

```
NAP5        Met Lys Met Leu Tyr Ala Ala Ile Met Phe Leu Leu Val
NAP6        Met Lys Met Leu Tyr Ala Ile Ala Ile Met Phe Leu Leu Val
NAPc2                                                   Leu Val
AceNAP5     Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu Phe Leu Ile
AceNAP7     Met Ser Thr Leu Tyr Val Ile Ala Ile Cys Leu Leu Leu Val
AceNAP4d1   Met Ala Val Leu Tyr Ser Val Ala Ile Ala Leu Leu Leu Val
AceNAP4d2
AduNAP4
AduNAP7d1   Met Arg Met Leu Tyr Leu Val Pro Ile Trp Leu Leu Leu Ile
AduNAP7d2
AduNAP5
HpoNAP5     Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Val Thr
```

# Figure 11-2

| Name | Sequence |
|---|---|
| NAP5 | Ser Leu Cys Ser Ala Arg Thr Val Arg Lys Ala Tyr Pro Glu |
| NAP6 | Ser Leu Cys Ser Thr Arg Thr Val Arg Lys Ala Tyr Pro Glu |
| NAPc2 | Ser Tyr Cys Ser Gly --- --- --- --- Lys Ala Thr Met Gln |
| AceNAP5 | Ser Gln Cys Asn Gly --- --- --- --- Lys Ala Phe Pro Lys |
| AceNAP7 | Ser Gln Cys Asn Gly --- --- --- --- Arg Thr Val Lys Lys |
| AceNAP4d1 | Ser Gln Cys Ser Gly Lys Pro Asn Asn Val Met Thr Asn Ala |
| AceNAP4d2 | Val Pro Ile |
| AduNAP4 | Lys |
| AduNAP7d1 | Ser Leu Cys Ser Gly --- --- --- --- Lys Ala Ala Lys Lys |
| AduNAP7d2 | Asp Glu |
| HpoNAP5 | Val Val Leu Ser Ala --- --- --- --- --- --- Lys Thr |

# Figure 11-3

```
                    1                                             2
NAP5       Cys Gly Glu Asn Glu Trp Leu Asp Asp Cys Gly Thr Gln
NAP6       Cys Gly Glu Asn Glu Trp Leu Asp Val Cys Gly Thr Lys
NAPc2      Cys Gly Glu Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys
AceNAP5    Cys Asp Val Asn Glu Arg Phe Glu Val Cys Gly Asn Leu
AceNAP7    Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly Asn Ala
AceNAP4d1  Cys Gly Leu Asn Glu Tyr Phe Ala Glu Cys Gly Asn Met
AceNAP4d2  Cys Gly Ser Asn Glu Arg Tyr Ser Asp Cys Gly Asn Asp
AduNAP4    Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr
AduNAP7d1  Cys Gly Leu Asn Glu Arg Leu Asp --- Cys Gly Asn Leu
AduNAP7d2  Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr
AduNAP5    Cys Gly Pro Asn Glu Glu Tyr Thr Glu Cys Gly Asn Tyr
HpoNAP5    Cys Gly Pro Asn Glu Glu Tyr Thr Glu Cys Gly Thr ---
```

# Figure 11-4

```
NAP5        Lys Pro Cys³ Glu Ala Lys Cys⁴ ---  ---  ---  Asn Glu Glu
NAP6        Lys Pro Cys  Glu Ala Lys Cys  ---  ---  ---  Ser Glu Glu
NAPc2       Glu ---  Cys  Asp Lys Lys Tyr  Asp Gly Val Glu Glu
AceNAP5     Lys Glu Cys  Glu Leu Lys Cys  ---  ---  ---  ---  ---  ---
AceNAP7     Lys Asp Cys  Glu Thr Lys Cys  ---  ---  Gly ---  ---  ---
AceNAP4d1   Lys Glu Cys  His Arg Lys Cys  Asn Glu Glu Asn Glu Glu
AceNAP4d2   Lys Gln Cys  Glu Arg Lys Cys  Asn Glu Asp Tyr Glu Lys
AduNAP4     Lys His Cys  Glu Leu Lys Cys  Asp Arg Glu Leu Thr Glu Lys
AduNAP7d1   Lys Gln Cys  Glu Pro Lys Cys  Ser Asp Leu Glu Ser Glu Glu
AduNAP7d2   Lys Lys Cys  Glu Arg Lys Cys  Ser Glu Glu Thr Ser Glu Lys
HpoNAP5     --- Pro Glu  Pro Lys Cys  ---  ---  ---  ---  ---  ---
```

# Figure 11-5

| Name | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NAP5 | Pro | Pro | Glu | Glu | Glu | Asp | Pro | Ile | --- | --- | Cys (5) | Arg | Ser | Arg |
| NAP6 | --- | --- | Glu | Glu | Glu | Asp | Pro | Ile | --- | --- | Cys | Arg | Ser | Phe |
| NAPc2 | --- | Glu | Asp | Asp | Glu | Glu | Pro | Asn | Val | Pro | Cys | Leu | Val | Arg |
| AceNAP5 | --- | Asp | Glu | Asp | Pro | Lys | Ile | --- | --- | --- | Cys | --- | Ser | Arg |
| AceNAP7 | --- | Glu | Glu | Glu | --- | --- | Lys | --- | Val | --- | Cys | Arg | Ser | Arg |
| AceNAP4d1 | Arg | --- | Asp | Glu | Glu | --- | Arg | Ile | Thr | Ala | Cys | Leu | Ile | Arg |
| AceNAP4d2 | Gly | --- | Asp | Glu | --- | --- | --- | --- | --- | Ala | Cys | Arg | Ser | His |
| AduNAP4 | --- | --- | Glu | Glu | --- | Gln | --- | --- | --- | Ala | Cys | Leu | Ser | Arg |
| AduNAP7d1 | Tyr | --- | Glu | Glu | Asp | Glu | Ser | Lys | --- | --- | Cys | Arg | Ser | Arg |
| AduNAP7d2 | Asn | --- | Glu | Glu | --- | --- | --- | --- | --- | Ala | Cys | Leu | Ser | Arg |
| HpoNAP5 | --- | --- | Asn | Glu | Pro | Met | Pro | Asp | Ile | --- | Cys | --- | Thr | Leu |

# Figure 11-6

```
                        6                              7     8
NAP5        Gly  Cys  Leu  Leu  Pro  Pro  Ala  Cys  Val  Cys  Lys  Asp
NAP6        Ser  Cys  Pro  Gly  Pro  Ala  Ala  Cys  Val  Cys  Glu  Asp
NAPc2       Val  Cys  His  Gln  Asp  ---  ---  Cys  Val  Cys  Glu  Glu
AceNAP5     Ala  Cys  Ile  Arg  Pro  Pro  Ala  Cys  Val  Cys  Asp  Asp
AceNAP7     Glu  Cys  Thr  Ser  Pro  Gly  Ala  Cys  Val  Cys  Glu  Gln
AceNAP4d1   Val  Cys  Phe  Arg  Pro  Gly  Ala  Cys  Val  Cys  Lys  Asp
AceNAP4d2   Val  Cys  Glu  Arg  Pro  Gly  Ala  Cys  Val  Cys  Glu  Asp
AduNAP4     Val  Cys  Glu  Lys  ---  Ser  Ala  Cys  Val  Cys  Asn  Asp
AduNAP7d1   Glu  Cys  Ser  Arg  Arg  ---  Val  Cys  Val  Cys  Asp  Glu
AduNAP7d2   Ala  Cys  Thr  Gly  Arg  ---  Ala  Cys  Val  Cys  Lys  Asp
HpoNAP5     Asn  Cys  Ile  Val  Asn  ---  Val  Cys  Gln  Cys  Lys  Pro
```

# Figure 11-7

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NAP5 | Gly | Phe | Tyr | Arg | Asp | Thr | Val | Ile | Gly | Asp | Cys | Val | Arg | Glu |
| NAP6 | Gly | Phe | Tyr | Arg | Asp | Thr | Val | Ile | Gly | Asp | Cys | Val | Lys | Glu |
| NAPc2 | Gly | Phe | Tyr | Arg | Asn | Lys | --- | Asp | Asp | Lys | Cys | Val | Ser | Ala |
| AceNAP5 | Gly | Phe | Tyr | Arg | Asp | Lys | Tyr | --- | Gly | Phe | Cys | Val | Glu | Glu |
| AceNAP7 | Gly | Phe | Tyr | Arg | Asp | Pro | Ala | --- | Gly | Asp | Cys | Val | Thr | Asp |
| AceNAP4d1 | Gly | Phe | Tyr | Arg | Asn | Arg | Thr | --- | Gly | Ser | Cys | Val | Glu | Glu |
| AceNAP4d2 | Gly | Phe | Tyr | Arg | Asn | Lys | Lys | --- | Gly | Ser | Cys | Val | Glu | Ser |
| AduNAP4 | Gly | Leu | Tyr | Arg | Asp | Lys | Phe | --- | Gly | Asn | Cys | Val | Glu | Lys |
| AduNAP7d1 | Gly | Phe | Tyr | Arg | Asn | Lys | Lys | --- | Gly | Lys | Cys | Val | Ala | Lys |
| AduNAP7d2 | Gly | Leu | Tyr | Arg | Asp | Asp | Phe | --- | Gly | Asn | Cys | Val | Pro | His |
| HpoNAP5 | Gly | Phe | Lys | Arg | Gly | Pro | Lys | --- | Gly | --- | Cys | Val | Ala | Pro |

# Figure 11-8

```
                                    1 0
NAP5        Glu Glu   Glu Glu ---  Cys  Asp Gln His --- --- Glu Ile Ile His
NAP6        Glu Glu   ---          Cys  Asp Gln His --- --- Glu Ile Ile His
NAPc2       Glu Asp   ---          Cys  Glu --- Leu Asp Asn Met Asp Phe Ile Tyr
AceNAP5     Asp Glu   ---          Cys  Asn Asp --- --- Met Glu Ile Ile Thr
AceNAP7     Glu Glu   ---          Cys  Asp Glu Trp Asn Asn Met Glu Ile Ile Thr
AceNAP4d1   Asp Asp   ---          Cys  Glu --- Tyr Glu Asn Met Glu Phe Ile Thr
AceNAP4d2   Asp Asp   ---          Cys  Glu --- Tyr Asp Asn Met Asp Phe Ile Thr
AduNAP4     Asp Glu   ---          Cys  Asn Asp --- --- Met Glu Ile Ile Thr
AduNAP7d1   Asp Val   ---          Cys  Glu Asp --- Asp Asn Met Glu Ile Ile Thr
AduNAP7d2   Asp Glu   ---          Cys  Asn Asp --- --- Met Glu Ile Ile Thr
HpoNAP5     Gly Pro Gly            Cys  Lys end
```

# Figure 11-9

| Name | Sequence |
|---|---|
| NAP5 | Val end |
| NAP6 | Val end |
| NAPc2 | Pro Gly Thr Arg Asn end |
| AceNAP5 | Phe Pro Pro Glu Thr Lys end |
| AceNAP7 | Met Pro Lys Gln end |
| AceNAP4d1 | Phe Ala Pro Glu |
| AceNAP4d2 | Phe Ala Pro Glu Thr Ser Arg end |
| AduNAP4 | Phe Ala Pro Glu Thr Lys end |
| AduNAP7d1 | Phe Pro Pro Glu |
| AduNAP7d2 | Phe Pro Pro Glu Thr Lys His end |
| HpoNAP5 | |

# Figure 12

## A
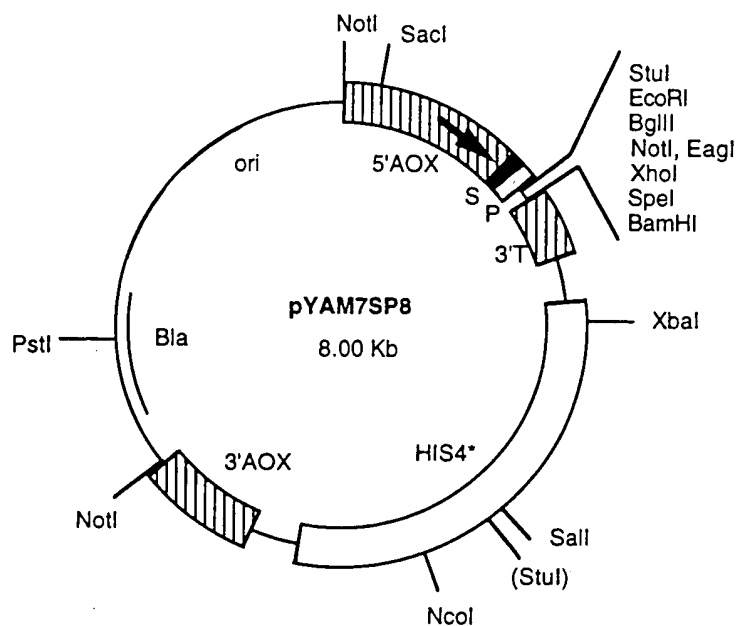


## B

```
<----5'AOX1-------><---------PHO1 secretion signal (S)--

......TTATTCGAAACGATGTTCTCTCCAATTTTGTCCTTGGAAATTATTTTA


------------------------><----Pro Sequence (P)----------

GCTACTTTGCAATCTGTCTTCGCCCAGCCAGTTATCTCCACTACCGTTGGTTCC


------------------------><-Multi-Cloning Site (MCS)

GCTGCCGAGGGTTCTTTGGACAAGAGGCCTATCCGCGGAATTCAGATCTGAAT
                        StuI    SacIIEcoRI BglII


------------------------><---3'T---->

GCGGCCGCTCGAGACTAGTGGATCCTTAGACA...
NotI   XhoI  SpeI  BamHI
 EagI
```

## Figure 13 A-1 (AcaNAP23)

```
            10            20            30            40
            *             *             *             *
  GAATTCCGCG GAATTCCGCT TGCTACTACT CAACG ATG AAG ACG CTC
  EcoRI                                  Met Lys Thr Leu

   50            60            70            80
   *             *             *             *
  TAT ATT GTC GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT
  Tyr Ile Val Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr

  90            100           110           120           130
  *             *             *             *             *
  GGA AAA CCT TCG GAG AAA GAA TGT GGT CCC CAT GAA AGA CTC
  Gly Lys Pro Ser Glu Lys Glu Cys Gly Pro His Glu Arg Leu
            140           150           160           170
            *             *             *             *
  GAC TGT GGC AAC AAG AAG CCA TGC GAG CGC AAG TGC AAA ATA
  Asp Cys Gly Asn Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile
            180           190           200           210
            *             *             *             *
  GAG ACA AGT GAG GAG GAG GAT GAC TAC GAA GAG GGA ACC GAA
  Glu Thr Ser Glu Glu Glu Asp Asp Tyr Glu Glu Gly Thr Glu

         220           230           240           250
         *             *             *             *
  CGT TTT CGA TGC CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA
  Arg Phe Arg Cys Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu

   260           270           280           290
   *             *             *             *
  TGC ATA TGC GAT GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA
  Cys Ile Cys Asp Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu

  300           310           320           330           340
  *             *             *             *             *
  TGT GTG ACT GAT GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT
  Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu Phe

            350           360           370           380
            *             *             *             *
  ATT ACT TTC GCA CCA TAA ACCCAATAAT GACCAATGAC TCCCATTCTT
  Ile Thr Phe Ala Pro
```

**Figure 13 A-2**

```
390         400         410         420         430
 *           *           *           *           *
CGTGATCAGC GTCGGTGGTT GACAGTCTCC CCTACATCTT AGTAGTTTTG

440         450         460         470         480
 *           *           *           *           *
CTTGATAATG TATACATAAA CTGTACTTTC TGAGATAGAA TAAAGCTCTC

490
 *
AACTAC poly(A)
```

**Figure 13 B-1 (AcaNAP24)**

```
              10              20              30              40
              *               *               *               *
      GAATTCCGCG GAATTCCGCA ACG ATG AAG ACG CTC TAT ATT ATC
      EcoRI                      Met Lys Thr Leu Tyr Ile Ile


          50              60              70              80
          *               *               *               *
  GCT ATA TGC TCG CTC CTC ATT TCG TTG TGT ACT GGA AGA CCG
  Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro


      90              100             110             120
      *               *               *               *
  GAA AAA AAG TGC GGT CCC GGT GAA AGA CTC GCC TGT GGC AAT
  Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Ala Cys Gly Asn


  130             140             150             160             170
  *               *               *               *               *
  AAG AAG CCA TGC GAG CGC AAG TGC AAA ATA GAG ACA AGT GAG
  Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu


          180             190             200             210
          *               *               *               *
  GAG GAG GAT GAC TAC CCA GAG GGA ACC GAA CGT TTT CGA TGC
  Glu Glu Asp Asp Tyr Pro Glu Gly Thr Glu Arg Phe Arg Cys


          220             230             240             250
          *               *               *               *
  CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA TGC ATA TGC GAT
  Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu Cys Ile Cys Asp


          260             270             280             290
          *               *               *               *
  GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT
  Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp


      300             310             320             330
      *               *               *               *
  GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA
  Asp Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala


  340         350         360         370         380
  *           *           *           *           *
  CCA TAA ACCCAATAAT GACCACTGGC TCCCATTCTT CGTGACCAGC
  Pro
```

**Figure 13 B-2**

```
        390          400          410          420          430
         *            *            *            *            *
     GTCGGTGGTT  GACAGTCTCC  CCTGCATCTT  AGTAGTTTTG  CTTGATAATG

        440          450          460          470
         *            *            *            *
     TATCCATAAA  CAGTACTTTC  TGAGATAGAA  TAAAGCTCTC  AACT poly(A)
```

**Figure 13 C (AcaNAP25)**

```
            10              20              30              40
            *               *               *               *
   GAATTCCGTA CTACTCAACG ATG AAG ACG CTC TAT ATT ATC GCT
   EcoRI                  Met Lys Thr Leu Tyr Ile Ile Ala

        50              60              70              80
        *               *               *               *
   ATA TGC TCG CTG CTC TTT TCA CTG TGT ACT GGA AGA CCG GAA
   Ile Cys Ser Leu Leu Phe Ser Leu Cys Thr Gly Arg Pro Glu

        90             100             110             120
        *               *               *               *
   AAA AAG TGC GGT CCC GGT GAA AGA CTC GAC TGT GCC AAC AAG
   Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn Lys

   130             140             150             160             170
   *               *               *               *               *
   AAG CCA TGC GAG CCC AAG TGC AAA ATA GAG ACA AGT GAG GAG
   Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu Glu

           180             190             200             210
           *               *               *               *
   GAG GAT GAC GAC GTA GAG GAT ACC GAT GTG AGA TGC CTC GTA
   Glu Asp Asp Asp Val Glu Asp Thr Asp Val Arg Cys Leu Val

       220             230             240             250
       *               *               *               *
   CGT GTG TGT GAA CGT CCT CTT AAA TGC ATA TGC AAG GAT GGA
   Arg Val Cys Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp Gly

       260             270             280             290
       *               *               *               *
   TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT GAT GTA
   Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp Asp Val

       300             310             320             330
       *               *               *               *
   TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA TAA
   Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro

   340        350        360        370        380
   *          *          *          *          *
   ACCCAATAAT GACCACTGGC TCCCATTCTT CGTGATCAGC GTCGGTGGTT

   390        400        410        420        430
   *          *          *          *          *
   GACAGTCTCC CCTGCATCTT AGTTGCTTTG CTTGATAATC TATACATAAA

   440        450        460        470
   *          *          *          *
   CAGTACTTTC TGAGATAGAA TAAAGCTCTC AACT poly(A)
```

Figure 13 D-1 (AcaNAP31)

```
           10          20          30          40          50
           *           *           *           *           *
  GAATTCCGGA CTTACTAGTA CTCAGCGAAT CAAATACGAC TTACTACTAC
  EcoRI

        60          70          80          90
        *           *           *           *
  TCAACG ATG AAG ACG CTC TCT GCT ATC CCT ATA ATG CTG CTC
         Met Lys Thr Leu Ser Ala Ile Pro Ile Met Leu Leu

        100         110         120         130
        *           *           *           *
  CTG GTA TCG CAA TGC AGT GGA AAA TCA CTG TGG GAT CAG AAG
  Leu Val Ser Gln Cys Ser Gly Lys Ser Leu Trp Asp Gln Lys

        140         150         160         170
        *           *           *           *
  TGT GGT GAG AAT GAA AGG CTC GAC TGT GGC AAT CAG AAG GAC
  Cys Gly Glu Asn Glu Arg Leu Asp Cys Gly Asn Gln Lys Asp

        180         190         200         210
        *           *           *           *
  TGT GAG CGC AAG TGC GAT GAT AAA AGA AGT GAA GAA GAA ATT
  Cys Glu Arg Lys Cys Asp Asp Lys Arg Ser Glu Glu Glu Ile

  220         230         240         250         260
  *           *           *           *           *
  ATG CAG GCA TGT CTC ACA CGT CAA TGT CTT CCT CCT GTT TGC
  Met Gln Ala Cys Leu Thr Arg Gln Cys Leu Pro Pro Val Cys

        270         280         290         300
        *           *           *           *
  GTA TGT GAA GAT GGA TTC TAC AGA AAT GAC AAC GAC CAA TGT
  Val Cys Glu Asp Gly Phe Tyr Arg Asn Asp Asn Asp Gln Cys

        310         320         330         340
        *           *           *           *
  GTT GAT GAA GAA GAA TGC AAT ATG GAG TTT ATT ACT TTC GCA
  Val Asp Glu Glu Glu Cys Asn Met Glu Phe Ile Thr Phe Ala

        350         360         370         380         390
        *           *           *           *           *
  CCA TGA AGCAAATGAC AGCCGATGGT TTGGACTCTC GCTACAGATC
  Pro

        400         410         420         430         440
        *           *           *           *           *
  ACAGCTTTAC TGTTTCCCTT GCATCATAGT AGTTTTGCTA GATAGTGTAT
```

**Figure 13 D-2**

```
        450           460           470           480
         *             *             *             *
ATATTAGCAT GATTTTCTGA TAGGGAGAAT AAAGCTTTCC AATTTTC
```

poly(A)

## Figure 13 E-1 (AcaNAP44)

```
          10            20              30              40
          *             *               *               *
  GAATTCCGCG GAATTCCGCA ACG ATG AAG ACG CTC TAT ATT ATC
  EcoRI                     Met Lys Thr Leu Tyr Ile Ile

        50              60            70              80
        *               *             *               *
  GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT GGA AGA CCG
  Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro

      90              100           110             120
      *               *             *               *
  GAA AAA AAG TGC GGT CCC GGT GAA AGA CTC GAC TGT GCC AAC
  Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn

 130             140           150             160            170
 *               *             *               *              *
  AAG AAG CCA TGC GAG CCC AAG TGC AAA ATA GAG ACA AGT GAG
  Lys Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu

           180             190           200             210
           *               *             *               *
  GAG GAG GAT GAC GAC GTA GAG GAA ACC GAT GTG AGA TGC CTC
  Glu Glu Asp Asp Asp Val Glu Glu Thr Asp Val Arg Cys Leu

        220             230           240             250
        *               *             *               *
  GTA CGT GTG TGT GAA CGG CCT CTT AAA TGC ATA TGC AAG GAT
  Val Arg Val Cys Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp

      260             270           280             290
      *               *             *               *
  GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT GAT
  Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp Asp

    300             310           320             330
    *               *             *             *
  GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA
  Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro

 340       350           360           370           380
 *         *             *             *             *
  TAA ACCCAATAAT GACCACTGGC TCCCATTCTT CGTGATCAGC

         390           400           410           420           430
         *             *             *             *             *
  GTCGGTGGTT GACAGTCTCC CCTGCATCTT AGTTGCTTTG CTTGATAATC
```

**Figure 13 E-2**

```
        440          450          460          470
         *            *            *            *
  TATACATAAA CAGTACTTTC TGAGATAGAA TAAAGCTCTC AACTAC

poly(A)
```

## Figure 13 F-1 (AcaNAP45)

```
              10                 20                30                40
               *                  *                 *                 *
     GAATTCCGGA AAA ATG CTG ATG CTC TAC CTT GTT CCT ATC TGG
     EcoRI          Met Leu Met Leu Tyr Leu Val Pro Ile Trp

           50                 60                70                80
            *                  *                 *                 *
     TTG CTA CTC ATT TCG CAA TGC AGT GGA AAA TCC GCG AAG AAA
     Leu Leu Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys Lys

           90                100               110               120
            *                  *                 *                 *
     TGT GGT CTC AAT GAA AAA TTG GAC TGT GGC AAT CTG AAG GCA
     Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala

     130                140               150               160
      *                  *                 *                 *
     TGC GAG AAA AAG TGC AGC GAC TTG GAC AAT GAG GAG GAT TAT
     Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp Tyr

     170                180               190               200               210
      *                  *                 *                 *                 *
     AAG GAG GAA GAT GAG TCG AAA TGC CGA TCA CGT GAA TGT AGT
     Lys Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser

              220                230               240               250
               *                  *                 *                 *
     CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC TAC AGA AAC AAG
     Arg Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys

              260                270               280               290
               *                  *                 *                 *
     AAG GGC CAA TGT GTG ACA AGA GAT GAT TGC GAG TAT GAC AAT
     Lys Gly Gln Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn

              300                310               320               330
               *                  *                 *                 *
     ATG GAG ATT ATC ACT TTT CCA CCA GAA GAT AAA TGT GGT CCC
     Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Lys Cys Gly Pro

     340                350               360               370
      *                  *                 *                 *
     GAT GAA TGG TTC GAC TGG TGT GGA ACT TAC AAG CAG TGT GAG
     Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys Gln Cys Glu

     380                390               400               410               420
      *                  *                 *                 *                 *
     CGC AAG TGC AAT AAG GAG CTA AGT GAG AAA GAT GAA GAG GCA
     Arg Lys Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Glu Ala
```

**Figure 13 F-2**

```
              430              440              450            460
               *                *                *             *
   TGC CTC TCA CGT GCT TGT ACT GGT CGT GCT TGT GTT TGC AAC
   Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys Asn

           470              480              490          500
            *                *                *           *
   GAC GGA CTG TAC AGA GAC GAT TTT GGC AAT TGT GTT GAG AAA
   Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Glu Lys

        510              520              530          540
         *                *                *            *
   GAC GAA TGT AAC GAT ATG GAG ATT ATC ACT TTT CCA CCG GAA
   Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu

   550              560          570          580
    *                *            *            *
   ACC AAA CAC TGA CCAAAGGCTC TAACTCTCGC TACATAACGT
   Thr Lys His

590          600          610          620          630
 *            *            *            *            *
   CAGTGCTTGA ATTGCCCCTT TACGAGTTAG TAATTTTGAC TAACTCTGTG

640          650          660          670          680
 *            *            *            *            *
   TAATTGAGCA TTGTCTACTG ATGGTGAAAA TGAAGTGTTC AATGTCT

   poly(A)
```

## Figure 13 G-1 (AcaNAP47)

```
              10          20          30          40
              *           *           *           *
      GAATTCCGCG GAATTCCGGT TGGCGGCAGA AAA ATG CTG ATG CTC
      EcoRI                              Met Leu Met Leu

          50          60          70          80
          *           *           *           *
      TAC CTT GTT CCT ATC TGG TTC CTG CTC ATT TCG CAA TGC AGT
      Tyr Leu Val Pro Ile Trp Phe Leu Leu Ile Ser Gln Cys Ser

          90         100         110         120
          *           *           *           *
      GGA AAA TCC GCG AAG AAA TGT GGC CTC AAT GAA AAA TTG GAC
      Gly Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp

     130         140         150         160         170
     *           *           *           *           *
      TGT GGC AAT CTG AAG GCA TGC GAG AAA AAG TGC AGC GAC TTG
      Cys Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu

              180         190         200         210
              *           *           *           *
      GAC AAT GAG GAG GAT TAT GGG GAG GAA GAT GAG TCG AAA TGC
      Asp Asn Glu Glu Asp Tyr Gly Glu Glu Asp Glu Ser Lys Cys

              220         230         240         250
              *           *           *           *
      CGA TCA CGT GAA TGT ATT GGT CGT GTT TGC GTA TGC GAT GAA
      Arg Ser Arg Glu Cys Ile Gly Arg Val Cys Val Cys Asp Glu

              260         270         280         290
              *           *           *           *
      GGA TTC TAC AGA AAC AAG AAG GGC CAA TGT GTG ACA AGA GAC
      Gly Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp

     300         310         320         330
     *           *           *           *
      GAT TGC GAG TAT GAC AAT ATG GAG ATT ATC ACT TTT CCA CCA
      Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro

     340         350         360         370         380
     *           *           *           *           *
      GAA GAT AAA TGT GGT CCC GAT GAA TGG TTC GAC TGG TGT GGA
      Glu Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly

              390         400         410         420
              *           *           *           *
      ACT TAC AAG CAG TGT GAG CGC AAG TGC AGT GAG GAG CTA AGT
      Thr Tyr Lys Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser
```

**Figure 13 G-2**

```
            430                440                450                460
             *                  *                  *                  *
    GAG AAA AAT GAG GAG GCA TGC CTC TCA CGT GCT TGT ACT GGT
    Glu Lys Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly

            470                480                490                500
             *                  *                  *                  *
    CGT GCT TGC GTT TGC AAC GAC GGA TTG TAT AGA GAC GAT TTT
    Arg Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Asp Phe

        510            520            530            540
         *              *              *              *
    GGC AAT TGT GTT GAG AAA GAC GAA TGT AAC GAT ATG GAG ATT
    Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile

    550            560            570            580
     *              *              *              *
    ATC ACT TTT CCA CCG GAA ACC AAA CAC TGA CCAAAGGCTC
    Ile Thr Phe Pro Pro Glu Thr Lys His

    590        600        610        620        630
     *          *          *          *          *
    TAGCTCTCGC TACATAACGT CAGTGCTTGA ATTGTCCCTT TACGTGTTAG

    640        650        660        670        680
     *          *          *          *          *
    TAATTTTGAC TAACTCTGTG TATTTGAGCA TTGTCTACTA ATGGTGAAAA

    690        700
     *          *
    TGAAGCTTTT CAATGACT poly(A)
```

## Figure 13 H-1 (AcaNAP48)

```
               10            20           30            40
                *             *            *             *
        GAATTCCGTA CGACCTACTA CTACTCAACG ATG AAG GCG CTC TAT
        EcoRI                           Met Lys Ala Leu Tyr


          50            60           70            80
           *             *            *             *
        GTT ATC TCT ATA ACG TTG CTC CTG GTA TGG CAA TGC AGT GCA
        Val Ile Ser Ile Thr Leu Leu Leu Val Trp Gln Cys Ser Ala


         90            100          110           120
          *             *            *             *
        AGA ACA GCG AGG AAA CCC CCA ACG TGT GGT GAA AAT GAA AGG
        Arg Thr Ala Arg Lys Pro Pro Thr Cys Gly Glu Asn Glu Arg


      130           140          150           160          170
        *             *            *            *             *
        GTC GAA TGG TGT GGC AAG CAG TGC GAG ATC ACA TGT GAC GAC
        Val Glu Trp Cys Gly Lys Gln Cys Glu Ile Thr Cys Asp Asp


              180           190          200           210
               *             *            *             *
        CCA GAT AAG ATA TGC CGC TCA CTC GCT TGT CCT GGT CCT CCT
        Pro Asp Lys Ile Cys Arg Ser Leu Ala Cys Pro Gly Pro Pro


            220           230          240           250
             *             *            *             *
        GCT TGC GTA TGC GAC GAC GGA TAC TAC AGA GAC ACG AAC GTT
        Ala Cys Val Cys Asp Asp Gly Tyr Tyr Arg Asp Thr Asn Val


          260           270          280           290
           *             *            *             *
        GGC TTG TGT GTA CAA TAT GAC GAA TGC AAC GAT ATG GAT ATT
        Gly Leu Cys Val Gln Tyr Asp Glu Cys Asn Asp Met Asp Ile


      300           310          320          330          340
        *             *            *            *             *
        ATT ATG GTT TCA TAG GGTTGACTGA AGAATCGAAC AACCGGTGCA
        Ile Met Val Ser


          350           360          370          380          390
           *             *            *            *             *
        CAACTTCTAT GCTTGACTAT CTCTCTTGCA TCATGCAAGT TTAGCTAGAT


          400           410          420          430          440
           *             *            *            *             *
        AGTGTATATA TTAGCAAGAC CCCTTGGGGA GAATGAAGCT TCCCAACTAT


          450           460          470          480          490
           *             *            *            *             *
        ATTAAATCAA TAACGTTTTC GCTTCATGTA CACGTGCTCA GCACATTCAT
```

**Figure 13 H-2**

```
        500            510          520
         *              *            *
ATCCACTCCT CACACTCCAT GAAAGCAGTG AAATGTT poly(A)
```

**Figure 14**

```
          10            20            30            40
           *             *             *             *
GCC AAC TCT TCG AAC ATG ATT CGA GGC CTC GTT CTT CTT TCT CTC CTG
                    Met Ile Arg Gly Leu Val Leu Leu Ser Leu Leu>


    50            60            70            80            90
     *             *             *             *             *
TTT TGC GTC ACT TTT GCA GCG AAG AGA GAT TGT CCA GCA AAT GAG GAA
Phe Cys Val Thr Phe Ala Ala Lys Arg Asp Cys Pro Ala Asn Glu Glu>


       100           110           120           130           140
        *             *             *             *             *
TGG AGG GAA TGT GGC ACT CCA TGT GAA CCA AAA TGC AAT CAA CCG ATG
Trp Arg Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Gln Pro Met>


          150           160           170           180           190
           *             *             *             *             *
CCA GAT ATA TGT ACT ATG AAT TGT ATC GTC GAT GTG TGT CAA TGC AAG
Pro Asp Ile Cys Thr Met Asn Cys Ile Val Asp Val Cys Gln Cys Lys>


       200           210           220           230           240
        *             *             *             *             *
GAG GGA TAC AAG CGT CAT GAA ACG AAG GGA TGC TTA AAG GAA GGA TCA
Glu Gly Tyr Lys Arg His Glu Thr Lys Gly Cys Leu Lys Glu Gly Ser>


       250           260           270           280
        *             *             *             *
GCT GAT TGT AAA TAA GTT ATC AGA ACG CTC GTT TTG TCT TAC ATT AGA
Ala Asp Cys Lys ***


  290           300           310           320           330
   *             *             *             *             *
TGG GTG AGC TGA TGT ATC TGT CAG ATA AAC TCT TTC TTC TAA AAA AAA


  340           350           360
   *             *             *
AAA AAA AAA AAA AAA AAA AAA AAA A
```
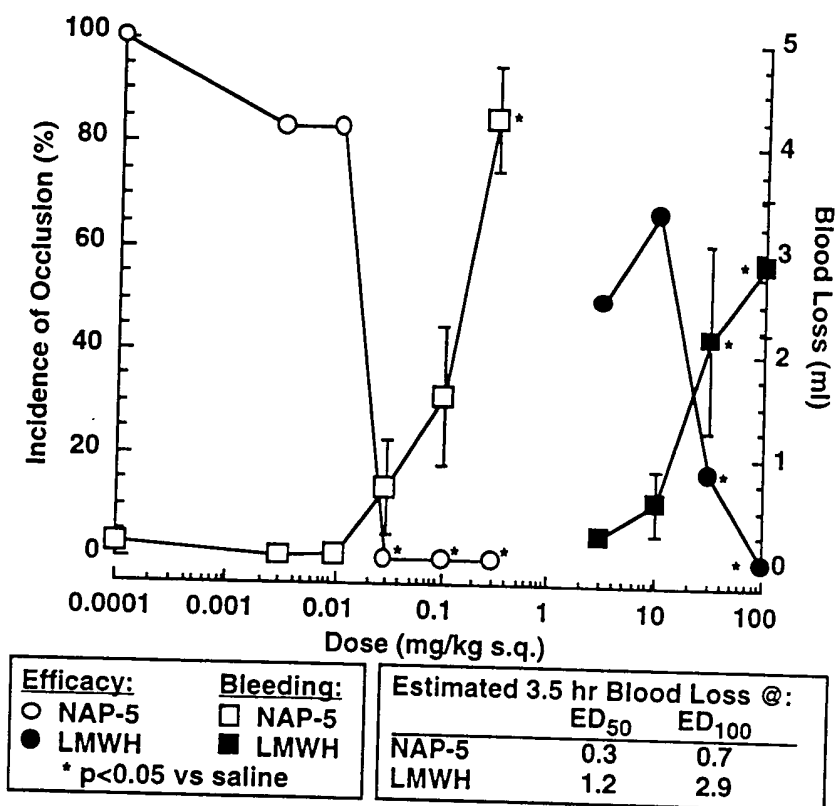
## FIGURE 15



| Efficacy: | Bleeding: |
|-----------|-----------|
| O  NAP-5 | ☐  NAP-5 |
| ●  LMWH | ■  LMWH |
| * p<0.05 vs saline | |

| Estimated 3.5 hr Blood Loss @: | | |
|------|------|------|
| | $ED_{50}$ | $ED_{100}$ |
| NAP-5 | 0.3 | 0.7 |
| LMWH | 1.2 | 2.9 |

## FIGURE 16

| | A1 | A2 | A3 | A4 | A5 | A6 | A7 | A8 | A9 | A10 |
|---|---|---|---|---|---|---|---|---|---|---|
| AcaNAP5 | KAYPECGE | NEMLDDC | GTYQKP | CEAKC NEEPPE | EE DPIC | RS RQCL LPP | ACVCK D | GFYRD TV | IGDCVR E EECDQ H | EIIHV |
| AcaNAP6 | KAYPECGE | NEMLDVC | GTYKP | CEAKC SEEE | EE DPIC | RS FSCP GPA | ACVCE D | GFYRD TV | IGDCVK E EECDQ H | EIIHV |
| AcaNAP48 | RTARKPPTCGE | NERVEMC | G KQ | CEITC DDP | DKIC | RS LACP GPP | ACVCD D | GYYRD TN | VGLCVQ Y DECND | MDIDMVS |
| AcaNAP23 | KPSEKDCGP | HERLD C | GNRKP | CERKC KIETSEEEDDYEEGTE | RFRC LL | RVCD QPY | BCICD D | GYYRN K | KGBCVT D DVCQE | DFMEFITFAP |
| AcaNAP24 | RPEKKCGP | GERLA C | GNRKP | CERKC KIETSEEEDDYPBGTE | RFRC LL | RVCD | BCICD D | GYYRN K | KGBCVT D DVCQE | DFMEFITFAP |
| AcaNAP25 | RPEKKCGP | GERLD C | GNRKP | CERKC KIETSEEEDDYE | DT DVRC LV | RVCE RPL | KCICK D | GYYRN K | KGBCVT D DVCQE | DFMEFITFAP |
| AcaNAP44 | RPEKKCGP | GERLD C | ANRKP | CERKC KIETSEEEDDVE | DT DVRC LV | RVCE RPL | KCICK D | GYYRN K | KGBCVT D DVCQE | DFMEFITFAP |
| AcaNAP31,42,46 | KSLWDQKCGE | NERLD C | GNQKD | CERKC KIETSEEFDDDVE | ET MQAC LT | RQCL PP | VCVCE D | GYYRN K | KGBCVT D DVCQE | DFMEFITFAP |
| AcaNAP4-d1 | KPNNVMTNACGL | NEYFABC | GNMRE | CEIHC NEE ENERDE | EI MQAC LT | RQCL PP | VCVCE D | GFYRN D | NDQCVD E EBCQN | MEFITFAP |
| AcaNAP4-d2 | VPICGS | NERYSDC | GNDKQ | CERKC NED DYEKG | ER ITAC LI | RVCF RPG | ACVCK D | GFYRN R | TGSCVE E DDCE | YENMEFITFAPE-> |
| AcaNAP45d1 | KSAKKCGL | NEKLD C | GNLKA | CEKKC SDL DNEEDYKE | ED ESKC | RS RECSR R | VCVCD E | GFYRN K | KGSCVE S DDCE | YDNMDFITFAPETSR |
| AcaNAP47d1 | KSAKKCGL | NEKLD C | GNLKA | CEKKC SDL DNEEDYGE | ED ESKC | RS RBCIG R | VCVCD E | GFYRN K | KGQCVT R DDCEY | DNMEIITFPPE-> |
| AduNAP7-d1 | KAAKKCGL | NERLD C | GNLKQ | CEPKC SDL ESEEYEE | ED ESKC | RS RBCS R R | VCVCD E | GFYRN K | KGQCVT R DDCEY | DNMEIITFPPE-> |
| AcaNAP45d2 | DKCGP | DEWFDWC | GTYKQ | CERKC NKE LSEKO | EEAC LS | RACTG R | ACVCN D | GFYRN K | KGKCVA K DVCED | DNMEIITFPPE-> |
| AcaNAP47d2 | DKGGP | DEWFDWC | GTYKQ | CERKC SEE LSERN | EEAC LS | RACTG R | ACVCN D | GLYRD D | FGNCVE K DECND | MEIITFPPETKH |
| AduNAP4 | RCPT | DEWFDWC | GTYKH | CELKC DRE LITEKE | EQAC LS | RVCE K S | ACVCN D | GLYRD D | FGNCVE K DECND | MEIITFPPETKH |
| AduNAP7-d2 | DECGP | DEWFDYC | GNYKK | CERKC SEE TSEKN | EEAC LS | RACT G R | ACVCN D | GLYRD D | FGNCVE K DECND | MEIITFAPEETK |
| AceNAP5 | KAFPKCDV | NERFEVC | GNLKE | CELKC D | ED PKIC S | RACI RPP | ACVCD D | GLYRD D | FGNCVP H DECND | MEIITFPPETKH |
| AceNAP7 | RTVKKCGK | NERYDDC | GNAKD | CETKC G | EE EKVC | RS RBCT SPG | ACVCE Q | GFYRD P | AGDCVT D EBCDE | WNNMEIIITMPKQ |
| AcaNAPc2 | KATMQCGE | NEKYDSC | GSKE | CDKKC KYDGVEEEDDE | EP NVPC | LV RVCH Q | DCVGE E | GFYRN K | DDKCVS A EDCEL | DNMDFIYPGTRN |
| HpoNAP5 | KTCGP | NEEYTEC | GTP | CEPKC NEPMPDI | C TLN | CI VNV | CQCK P | GFKRGPKG | CVA PGPGC K | GYKRHETKG |
| NamNAP | KRDCPA | NEEWREC | GTP | CEPKC NQPMPDI | C TWN | CI VDV | CQCK E | GYKRHETKG | CLKBGSADC K | |

NAP = nematode anticoagulant protein

Aca = Ancyclostoma caninum
Ace = Ancyclostoma ceylanium
Adu = Ancyclostoma duodenale
Hpo = Heligmosmoides polygyrus
Asu = Ascaris suum
Nam = Necator americanus

# Figure 17

```
Lys Pro Asn Asn Val Met Thr Asn Ala Cys Gly Leu Asn Glu
1               5                   10

Tyr Phe Ala Glu Cys Gly Asn Met Lys Glu Cys Glu His Arg
15              20                  25

Cys Asn Glu Glu Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile
    30                  35                  40

Thr Ala Cys Leu Ile Arg Val Cys Phe Arg Pro Gly Ala Cys
        45          50                  55
Val Cys Lys Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser Cys
            60                  65                  70

Val Glu Glu Asp Asp Cys Glu Tyr Glu Asn Met Glu Phe Ile
                75                  80

Thr Phe Ala Pro Glu Val Pro Ile Cys Gly Ser Asn Glu Arg
85                  90              95

Tyr Ser Asp Cys Gly Asn Asp Lys Gln Cys Glu Arg Lys Cys
    100             105                 110

Asn Glu Asp Asp Tyr Glu Lys Gly Asp Glu Ala Cys Arg Ser
        115             120                 125

His Val Cys Glu Arg Pro Gly Ala Cys Val Cys Glu Asp Gly
        130                 135             140

Phe Tyr Arg Asn Lys Lys Gly Ser Cys Val Glu Ser Asp Asp
                145             150

Cys Glu Tyr Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu
155             160                 165

Thr Ser Arg
170
```

# Figure 18

```
Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys
1               5               10
```

```
Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp
15              20              25
```

```
Asn Glu Glu Asp Tyr Lys Glu Glu Asp Glu Ser Lys Cys Arg
    30              35              40
```

```
Ser Arg Glu Cys Ser Arg Arg Val Cys Val Cys Asp Glu Gly
        45          50          55
```

```
Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp Asp
            60          65              70
```

```
Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
            75          80
```

```
Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly Thr
85              90          95
```

```
Tyr Lys Gln Cys Glu Arg Lys Cys Asn Lys Glu Leu Ser Glu
    100         105             110
```

```
Lys Asp Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg
    115             120         125
```

```
Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly
        130         135             140
```

```
Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile Ile
            145             150
```

```
Thr Phe Pro Pro Glu Thr Lys His
155             160
```

# Figure 19

```
Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp Cys
1               5                   10

Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu Asp
15              20              25

Asn Glu Glu Asp Tyr Gly Glu Glu Asp Glu Ser Lys Cys Arg
    30              35              40

Ser Arg Glu Cys Ile Gly Arg Val Cys Val Cys Asp Glu Gly
        45          50              55

Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp Asp
            60              65                      70

Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
                75                  80

Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly Thr
85              90                  95

Tyr Lys Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser Glu
    100             105                 110

Lys Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg
        115             120             125

Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly
            130             135                 140

Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile Ile
                145             150

Thr Phe Pro Pro Glu Thr Lys His
155                 160
```

# Figure 20

```
Lys Ala Ala Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys
1               5               10
```

```
Gly Asn Leu Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu
15              20              25
```

```
Ser Glu Glu Tyr Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser
    30              35              40
```

```
Arg Glu Cys Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe
        45          50      55
```

```
Tyr Arg Asn Lys Lys Gly Lys Cys Val Ala Lys Asp Val Cys
            60          65              70
```

```
Glu Asp Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp
                75              80
```

```
Glu Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr
85              90              95
```

```
Lys Lys Cys Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys
    100             105                 110
```

```
Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala
        115             120             125
```

```
Cys Val Cys Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn
        130             135             140
```

```
Cys Val Pro His Asp Glu Cys Asn Asp Met Glu Ile Ile Thr
                145             150
```

```
Phe Pro Pro Glu Thr Lys His
155             160
```